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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/849,868

DATE: 06/05/2001

TIME: 13:11:28

Input Set : A:\seqlist.txt

Output Set: C:\CRF3\06052001\I849868.raw

ENTERED

4 <110> APPLICANT: Genentech, Inc.
 5 Gao, Wei-Qiang
 7 <120> TITLE OF INVENTION: HAIR CELL DISORDERS
 10 <130> FILE REFERENCE: GENENT.035VPC
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/849,868
 C--> 12 <141> CURRENT FILING DATE: 2001-05-04
 12 <160> NUMBER OF SEQ ID NOS: 14
 14 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 669
 18 <212> TYPE: PRT
 19 <213> ORGANISM: Homo sapiens
 21 <400> SEQUENCE: 1
 22 Ala Arg Ala Pro Gln Arg Gly Arg Ser Leu Ser Pro Ser Arg Asp Lys
 23 1 5 10 15
 24 Leu Phe Pro Asn Pro Ile Arg Ala Leu Gly Pro Asn Ser Pro Ala Pro
 25 20 25 30
 26 Arg Ala Val Arg Val Glu Arg Ser Val Ser Gly Glu Met Ser Glu Arg
 27 35 40 45
 28 Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys Glu Arg Gly Ser
 29 50 55 60
 30 Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser Pro Ala Leu Pro
 31 65 70 75 80
 32 Pro Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Ala Ala Gly Ser Lys
 33 85 90 95
 34 Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Arg Phe
 35 100 105 110
 36 Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys Asn Lys Pro Gln
 37 115 120 125
 38 Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg Ile Asn
 39 130 135 140
 40 Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser
 41 145 150 155 160
 42 Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser
 43 165 170 175
 44 Asn Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu Gly Ala Tyr Val
 45 180 185 190
 46 Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Ala Asn
 47 195 200 205
 48 Thr Ser Ser Ser Thr Ser Thr Ser Thr Thr Gly Thr Ser His Leu Val
 49 210 215 220
 50 Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys
 51 225 230 235 240
 52 Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys
 53 245 250 255
 54 Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn Val Pro Met Lys
 55 260 265 270

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56 Val Gln Asn Gln Glu Lys Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu
57      275      280      285
58 Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val Val Gly Ile Met Cys
59      290      295      300
60 Val Val Ala Tyr Cys Lys Thr Lys Lys Gln Arg Lys Lys Leu His Asp
61 305      310      315      320
62 Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn Asn Met Met Asn Ile
63      325      330      335
64 Ala Asn Gly Pro His His Pro Asn Pro Pro Pro Glu Asn Val Gln Leu
65      340      345      350
66 Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser Ser Glu His Ile Val
67      355      360      365
68 Glu Arg Glu Ala Glu Thr Ser Phe Ser Thr Ser His Tyr Thr Ser Thr
69      370      375      380
70 Ala His His Ser Thr Thr Val Thr Gln Thr Pro Ser His Ser Trp Ser
71 385      390      395      400
72 Asn Gly His Thr Glu Ser Ile Leu Ser Glu Ser His Ser Val Ile Val
73      405      410      415
74 Met Ser Ser Val Glu Asn Ser Arg His Ser Ser Pro Thr Gly Gly Pro
75      420      425      430
76 Arg Gly Arg Leu Asn Gly Thr Gly Gly Pro Arg Glu Cys Asn Ser Phe
77      435      440      445
78 Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro His
79      450      455      460
80 Ser Glu Arg Tyr Val Ser Ala Met Thr Thr Pro Ala Arg Met Ser Pro
81 465      470      475      480
82 Val Asp Phe His Thr Pro Ser Ser Pro Lys Ser Pro Pro Ser Glu Met
83      485      490      495
84 Ser Pro Pro Val Ser Ser Met Thr Val Ser Met Pro Ser Met Ala Val
85      500      505      510
86 Ser Pro Phe Met Glu Glu Glu Arg Pro Leu Leu Leu Val Thr Pro Pro
87      515      520      525
88 Arg Leu Arg Glu Lys Lys Phe Asp His His Pro Gln Gln Phe Ser Ser
89      530      535      540
90 Phe His His Asn Pro Ala His Asp Ser Asn Ser Leu Pro Ala Ser Pro
91 545      550      555      560
92 Leu Arg Ile Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln Glu Tyr Glu
93      565      570      575
94 Pro Ala Gln Glu Pro Val Lys Lys Leu Ala Asn Ser Arg Arg Ala Lys
95      580      585      590
96 Arg Thr Lys Pro Asn Gly His Ile Ala Asn Arg Leu Glu Val Asp Ser
97      595      600      605
98 Asn Thr Ser Ser Gln Ser Ser Asn Ser Glu Ser Glu Thr Glu Asp Glu
99      610      615      620
100 Arg Val Gly Glu Asp Thr Pro Phe Leu Gly Ile Gln Asn Pro Leu Ala
101 625      630      635      640
102 Ala Ser Leu Glu Ala Thr Pro Ala Phe Arg Leu Ala Asp Ser Arg Thr
103      645      650      655
104 Asn Pro Ala Gly Arg Phe Ser Thr Gln Glu Glu Ile Gln

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105          660          665
108 <210> SEQ ID NO: 2
109 <211> LENGTH: 2226
110 <212> TYPE: DNA
111 <213> ORGANISM: Homo sapiens
113 <220> FEATURE:
114 <221> NAME/KEY: CDS
115 <222> LOCATION: (2)...(2008)
117 <400> SEQUENCE: 2
118 g ggc gcg agc gcc tca gcg cgg ccg ctc gct ctc ccc ctc gag gga caa 49
119   Gly Ala Ser Ala Ser Ala Arg Pro Leu Ala Leu Pro Leu Glu Gly Gln
120     1          5          10          15
122 act ttt ccc aaa ccc gat ccg agc cct tgg acc aaa ctc gcc tgc gcc 97
123 Thr Phe Pro Lys Pro Asp Pro Ser Pro Trp Thr Lys Leu Ala Cys Ala
124           20           25           30
126 gag agc cgt ccg cgt aga gcg ctc cgt ctc cgg cga gat gtc cga gcg 145
127 Glu Ser Arg Pro Arg Arg Ala Leu Arg Leu Arg Arg Asp Val Arg Ala
128           35           40           45
130 caa aga agg cag agg caa agg gaa ggg caa gaa gaa gga gcg agg ctc 193
131 Gln Arg Arg Gln Arg Gln Arg Glu Gly Gln Glu Glu Gly Ala Arg Leu
132           50           55           60
134 cgg caa gaa gcc gga gtc cgc ggc ggg cag cca gag ccc agc ctt gcc 241
135 Arg Gln Glu Ala Gly Val Arg Gly Gly Gln Pro Glu Pro Ser Leu Ala
136    65           70           75           80
138 tcc ccg att gaa aga gat gaa aag cca gga atc ggc tgc agg ttc caa 289
139 Ser Pro Ile Glu Arg Asp Glu Lys Pro Gly Ile Gly Cys Arg Phe Gln
140           85           90           95
142 act agt cct tcg gtg tga aac cag ttc tga ata ctc ctc tct cag att 337
143 Thr Ser Pro Ser Val * Asn Gln Phe * Ile Leu Leu Ser Gln Ile
144           100          105          110
146 caa gtg gtt caa gaa tgg gaa tga att gaa tcg aaa aaa caa acc aca 385
147 Gln Val Val Gln Glu Trp Glu * Ile Glu Ser Lys Lys Gln Thr Thr
148           115          120          125
150 aaa tat caa gat aca aaa aaa gcc agg gaa gtc aga act tcg cat taa 433
151 Lys Tyr Gln Asp Thr Lys Lys Ala Arg Glu Val Arg Thr Ser His *
152           130          135          140
154 caa agc atc act ggc tga ttc tgg aga gta tat gtg caa agt gat cag 481
155 Gln Ser Ile Thr Gly * Phe Trp Arg Val Tyr Val Gln Ser Asp Gln
156           145          150          155
158 caa att agg aaa tga cag tgc ctc tgc caa tat cac cat cgt gga atc 529
159 Gln Ile Arg Lys * Gln Cys Leu Cys Gln Tyr His His Arg Gly Ile
160           160          165          170
162 aaa cga gat cat cac tgg tat gcc agc ctc aac tga agg agc ata tgt 577
163 Lys Arg Asp His His Trp Tyr Ala Ser Leu Asn * Arg Ser Ile Cys
164           175          180          185
166 gtc ttc aga gtc tcc cat tag aat atc agt atc cac aga agg agc aaa 625
167 Val Phe Arg Val Ser His * Asn Ile Ser Ile His Arg Arg Ser Lys
168           190          195          200
170 tac ttc ttc atc tac atc tac atc cac cac tgg gac aag cca tct tgt 673

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171	Tyr	Phe	Phe	Ile	Tyr	Ile	Tyr	Ile	His	His	Trp	Asp	Lys	Pro	Ser	Cys	
172				205					210					215			
174	aaa	atg	tgc	gga	gaa	gga	gaa	aac	ttt	ctg	tgt	gaa	tgg	agg	gga	gtg	721
175	Lys	Met	Cys	Gly	Glu	Gly	Glu	Asn	Phe	Leu	Cys	Glu	Trp	Arg	Gly	Val	
176				220				225					230				
178	ctt	cat	ggt	gaa	aga	cct	ttc	aaa	ccc	ctc	gag	ata	ctt	gtg	caa	gtg	769
179	Leu	His	Gly	Glu	Arg	Pro	Phe	Lys	Pro	Leu	Glu	Ile	Leu	Val	Gln	Val	
180			235					240					245				
182	cca	acc	tgg	att	cac	tgg	agc	aag	atg	tac	tga	gaa	tgt	gcc	cat	gaa	817
183	Pro	Thr	Trp	Ile	His	Trp	Ser	Lys	Met	Tyr	*	Glu	Cys	Ala	His	Glu	
184		250					255						260				
186	agt	cca	aaa	cca	aga	aaa	ggc	gga	gga	gct	gta	cca	gaa	gag	agt	gct	865
187	Ser	Pro	Lys	Pro	Arg	Lys	Gly	Gly	Gly	Ala	Val	Pro	Glu	Glu	Ser	Ala	
188		265					270						275				
190	gac	cat	aac	cgg	cat	ctg	cat	cgc	cct	cct	tgt	ggt	cgg	cat	cat	gtg	913
191	Asp	His	Asn	Arg	His	Leu	His	Arg	Pro	Pro	Cys	Gly	Arg	His	His	Val	
192	280					285					290					295	
194	tgt	ggt	ggc	cta	ctg	caa	aac	caa	gaa	aca	gcg	gaa	aaa	gct	gca	tga	961
195	Cys	Gly	Gly	Leu	Leu	Gln	Asn	Gln	Glu	Thr	Ala	Glu	Lys	Ala	Ala	*	
196				300					305					310			
198	ccg	tct	tcg	gca	gag	cct	tcg	gtc	tga	acg	aaa	caa	tat	gat	gaa	cat	1009
199	Pro	Ser	Ser	Ala	Glu	Pro	Ser	Val	*	Thr	Lys	Gln	Tyr	Asp	Glu	His	
200				315							320				325		
202	tgc	caa	tgg	gcc	tca	cca	tcc	taa	ccc	acc	ccc	cga	gaa	tgt	cca	gct	1057
203	Cys	Gln	Trp	Ala	Ser	Pro	Ser	*	Pro	Thr	Pro	Arg	Glu	Cys	Pro	Ala	
204				330							335				340		
206	ggt	gaa	tca	ata	cgt	atc	taa	aaa	cgt	cat	ctc	cag	tga	gca	tat	tgt	1105
207	Gly	Glu	Ser	Ile	Arg	Ile	*	Lys	Arg	His	Leu	Gln	*	Ala	Tyr	Cys	
208				345							350						
210	tga	gag	aga	agc	aga	gac	atc	ctt	ttc	cac	cag	tca	cta	tac	ttc	cac	1153
211	*	Glu	Arg	Ser	Arg	Asp	Ile	Leu	Phe	His	Gln	Ser	Leu	Tyr	Phe	His	
212		355				360					365						
214	agc	cca	tca	ctc	cac	tac	tgt	cac	cca	gac	tcc	tag	cca	cag	ctg	gag	1201
215	Ser	Pro	Ser	Leu	His	Tyr	Cys	His	Pro	Asp	Ser	*	Pro	Gln	Leu	Glu	
216	370					375					380						
218	caa	cgg	aca	cac	tga	aag	cat	cct	ttc	cga	aag	cca	ctc	tgt	aat	cgt	1249
219	Gln	Arg	Thr	His	*	Lys	His	Pro	Phe	Arg	Lys	Pro	Leu	Cys	Asn	Arg	
220	385					390					395						
222	gat	gtc	atc	cgt	aga	aaa	cag	tag	gca	cag	cag	ccc	aac	tgg	ggg	ccc	1297
223	Asp	Val	Ile	Arg	Arg	Lys	Gln	*	Ala	Gln	Gln	Pro	Asn	Trp	Gly	Pro	
224	400					405					410						
226	aag	agg	acg	tct	taa	tgg	cac	agg	agg	ccc	tcg	tga	atg	taa	cag	ctt	1345
227	Lys	Arg	Thr	Ser	*	Trp	His	Arg	Arg	Pro	Ser	*	Met	*	Gln	Leu	
228	415					420					425						
230	cct	cag	gca	tgc	cag	aga	aac	ccc	tga	ttc	cta	ccg	aga	ctc	tcc	tca	1393
231	Pro	Gln	Ala	Cys	Gln	Arg	Asn	Pro	*	Phe	Leu	Pro	Arg	Leu	Ser	Ser	
232			430					435						440			
234	tag	tga	aag	gta	tgt	gtc	agc	cat	gac	cac	ccc	ggc	tcg	tat	gtc	acc	1441
235	*	*	Lys	Val	Cys	Val	Ser	His	Asp	His	Pro	Gly	Ser	Tyr	Val	Thr	

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236          445          450          455
238 tgt aga ttt cca cac gcc aag ctc ccc caa atc gcc ccc ttc gga aat 1489
239 Cys Arg Phe Pro His Ala Lys Leu Pro Gln Ile Ala Pro Phe Gly Asn
240          460          465          470
242 gtc tcc acc cgt gtc cag cat gac ggt gtc cat gcc ttc cat ggc ggt 1537
243 Val Ser Thr Arg Val Gln His Asp Gly Val His Ala Phe His Gly Gly
244          475          480          485
246 cag ccc ctt cat gga aga aga gag acc tct act tct cgt gac acc acc 1585
247 Gln Pro Leu His Gly Arg Arg Glu Thr Ser Thr Ser Arg Asp Thr Thr
248          490          495          500
250 aag gct gcg gga gaa gaa gtt tga cca tca ccc tca gca gtt cag ctc 1633
251 Lys Ala Ala Gly Glu Glu Val * Pro Ser Pro Ser Ala Val Gln Leu
252 505          510          515
254 ctt cca cca caa ccc cgc gca tga cag taa cag cct ccc tgc tag ccc 1681
255 Leu Pro Pro Gln Pro Arg Ala * Gln * Gln Pro Pro Cys * Pro
256 520          525          530
258 ctt gag gat agt gga gga tga gga gta tga aac gac cca aga gta cga 1729
259 Leu Glu Asp Ser Gly Gly * Gly Val * Asn Asp Pro Arg Val Arg
260          535          540          545
262 gcc agc cca aga gcc tgt taa gaa act cgc caa tag ccg gcg ggc caa 1777
263 Ala Ser Pro Arg Ala Cys * Glu Thr Arg Gln * Pro Ala Gly Gln
264          550          555          560
266 aag aac caa gcc caa tgg cca cat tgc taa cag att gga agt gga cag 1825
267 Lys Asn Gln Ala Gln Trp Pro His Cys * Gln Ile Gly Ser Gly Gln
268          565          570          575
270 caa cac aag ctc cca gag cag taa ctc aga gag tga aac aga aga tga 1873
271 Gln His Lys Leu Pro Glu Gln * Leu Arg Glu * Asn Arg Arg *
272          580          585
274 aag agt agg tga aga tac gcc ttt cct ggg cat aca gaa ccc cct ggc 1921
275 Lys Ser Arg * Arg Tyr Ala Phe Pro Gly His Thr Glu Pro Pro Gly
276          590          595          600
278 agc cag tct tga ggc aac acc tgc ctt ccg cct ggc tga cag cag gac 1969
279 Ser Gln Ser * Gly Asn Thr Cys Leu Pro Pro Gly * Gln Gln Asp
280          605          610          615
282 taa ccc agc agg ccg ctt ctc gac aca gga aga aat cca ggccaggctg 2018
283 * Pro Ser Arg Pro Leu Leu Asp Thr Gly Arg Asn Pro
284          620          625
286 tctagtgttaa ttgctaacca agaccctatt gctgtataaa acctaaataa acacatagat 2078
287 tcacctgttaa aactttatitt tatataataa agtattccac cttaaattaa acaatttatt 2138
288 ttatttttagc agttctgcaa atagaaaaca ggaaaaaac ttttataaat taaatatatg 2198
289 tatgtaaaaa tgaaaaaaa aaaaaaaa 2226
291 <210> SEQ ID NO: 3
292 <211> LENGTH: 675
293 <212> TYPE: PRT
294 <213> ORGANISM: Homo sapiens
296 <400> SEQUENCE: 3
297 Asp Lys Leu Phe Pro Asn Pro Ile Arg Ala Leu Gly Pro Asn Ser Pro
298 1 5 10 15
299 Ala Pro Arg Ala Val Arg Val Glu Arg Ser Val Ser Gly Glu Met Ser

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VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date